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## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

**In re Application of:**

Boot et al.

**Serial No.:** 10/046,671**Filed:** January 14, 2002**For:** MOSAIC INFECTIOUS BURSAL  
DISEASE VIRUS VACCINES**Examiner:** To be assigned**Group Art Unit:** 1642**Attorney Docket No.:** 2183-5238USCERTIFICATE OF MAILING

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*Lynette Eliason*  
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Washington, D.C. 20231

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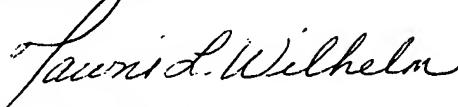
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Serial No.: 10/046,671

3. The SEQUENCE LISTING submitted herewith is believed to contain no "new matter" with regard to the referenced patent application.

Respectfully submitted,



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ACT/TLW/sw



#3

# SEQUENCE LISTING

<110> Hendrik J.  
Huurne ter, Anna A.H.M  
Peeters, Bernardus P.H.

<120> Mosaic Infectious Bursal Disease Virus Vaccines

<130> 2183-5238US

<140> US 10/046,671  
<141> 2002-01-14

<150> PCT/NL00/00493  
<151> 2000-07-13

<150> EP 99202316.8  
<151> 1999-07-14

<160> 87

<170> PatentIn Ver. 2.1

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 5123, 96-C6, 97-B4, 97-B5, 97-B6, Hungary, OKYM,  
 TKSM and HK46

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 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
 35 40 45  
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
 50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
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Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
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Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr  
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
65 70 75 80

Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
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Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
100 105 110

Gly Asp Gln Met Ser Trp Ser  
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 Ile Gly Gly Glu Leu Val Phe Asn Thr Ser Val Gln Gly Leu Ala Leu  
 35 40 45  
 Asn Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr  
 50 55 60  
 Arg Ala Val Ala Ser Asp Asn Gly Leu Thr Thr Gly Ile Asp Asn Leu  
 65 70 75 80  
 Met Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
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 Gly Asp Gln Met Ser Trp Ser  
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 Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu  
 35 40 45  
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr

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 Arg Ala Val Ala Ala Tyr Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
 65                      70                      75                      80  
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
                     85                      90                      95  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
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 Gly Asp Gln Met Ser Trp Ser  
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                     20                      25                      30  
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
                     35                      40                      45  
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
                     50                      55                      60  
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
 65                      70                      75                      80  
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
                     85                      90                      95  
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 Gly Asp Gln Met Ser Trp Ser  
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<210> 66  
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<213> Infectious bursal disease virus

<220>

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<222> (1)..(119)

<223> Amino acid sequence of the hypervariable  
region of VP2 of IBDV isolate Zoontjes

<400> 66

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
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Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Thr Thr Gln Pro Ile  
85 90 95

Thr Ser Ile Lys Leu Val Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
100 105 110

Gly Asp Gln Met Ser Trp Ser  
115

<210> 67

<211> 119

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable  
region of VP2 of IBDV isolate OKYMT

<400> 67

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Thr Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
 50 55 60  
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
 65 70 75 80  
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
 85 90 95  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Phe Lys Ser Gly Gly Gln Ala  
 100 105 110  
 Gly Asp Gln Met Ser Trp Ser  
 115

<210> 68  
 <211> 119  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(119)  
 <223> Amino acid sequence of the hypervariable  
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<400> 68  
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 Ile Gly Gly Glu Leu Val Phe His Thr Ser Val Gln Gly Leu Ile Leu  
 35 40 45  
 Asp Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Thr Thr  
 50 55 60  
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
 65 70 75 80  
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 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
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 Gly Asp Gln Met Ser Trp Ser  
 115

<210> 69  
 <211> 119

<212> PRT  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> DOMAIN  
 <222> (1)..(119)  
 <223> Amino acid sequence of the hypervariable  
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 <400> 69  
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             20                    25                    30  
  
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
             35                    40                    45  
  
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
             50                    55                    60  
  
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
     65                    70                    75                    80  
  
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
             85                    90                    95  
  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
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 Gly Asp Gln Met Ser Trp Ser  
     115

<210> 70  
 <211> 3260  
 <212> DNA  
 <213> Infectious bursal disease virus

<220>  
 <221> misc\_feature  
 <222> (1)..(3260)  
 <223> Consensus cDNA sequence of IBDV A-segment

<400> 70  
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<210> 71  
 <211> 3260  
 <212> DNA  
 <213> Infectious bursal disease virus

<220>  
 <221> misc\_feature

<222> (1)..(3260)

<223> cDNA sequence CEF94-A of IBV A-segment

<400> 71

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<210> 72

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc\_feature

<222> (1)..(3260)

<223> cDNA sequence D6948-A of IBV A-segment

<400> 72

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<210> 73

<211> 964

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc\_feature

<222> (1)..(964)

<223> cDNA sequence TY89-A of IBV A-segment

<400> 73

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<210> 74

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc\_feature  
 <222> (1)..(2827)  
 <223> Consensus cDNA sequence of IBDV B-segment

<400> 74

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rttttca aya gtccac aggc gcgaag camg atmtcag cag cgttcg gcat aaagcc tacw 180
gctggac arg aygtgga aga actcyt gatc cctaarg tyt gggtgcc acc tgaggat ccs 240
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caggagt act tcccwa arta ctacca aaca caycgcc cka gcaagg araa gcccaat gcg 480
taccgc ccmg ayatcg cayt actcaag cag atgatyt acy tgtttct cca ggttcc mgag 540
gccamm gakr rcctwa arga tgargtm acc ctmytra ccc aaaacat wag rgayaar gcc 600
tayggr agtg ggacct acat gggacarg cm acymgact tg tkgyat gaa rgaggty gcc 660
actggr agaa acccaa acaa rgatcct cta aagctt gggg acacyttt ga gagcat mgcs 720
cagctact tg acatcac wyt accggt aggc ccaccgg tg aggatg acaa gccctg ggtr 780
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gaggcg ttga ggttggt agg tggttgga ac taccact cc tgaacaa agc ytgcaaga ay 2040
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gccgtgaaaa tggccaaamg gcggcaac gc caaaarg aga gccgcca aya gccatgat gg 2760
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ggcccccc 2827

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<210> 75  
 <211> 2827  
 <212> DNA  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> misc\_feature  
 <222> (1)..(2827)  
 <223> cDNA sequence CEF94-B of IBDV B-segment

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<210> 76
<211> 2827
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(2827)
<223> cDNA sequence D6948-B of IBV B-segment

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2827

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<210> 77

<211> 1012

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(1012)

<223> Consensus sequence of IBDV polyprotein, whereby the Xaa indicator may be any amino acid

<400> 77

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Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
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```

```

Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
      20             25             30

```

```

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
    35             40             45

```

```

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
    50             55             60

```

```

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
    65             70             75             80

```

```

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
      85             90             95

```

```

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
    100            105            110

```

```

Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
    115            120            125

```

```

Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
    130            135            140

```

```

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
    145            150            155            160

```

```

Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly

```





Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
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 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
 485 490 495  
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
 500 505 510  
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln  
 515 520 525  
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Xaa Leu Arg Gly  
 530 535 540  
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro  
 545 550 555 560  
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn  
 565 570 575  
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro  
 580 585 590  
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val  
 595 600 605  
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp  
 610 615 620  
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu  
 625 630 635 640  
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala  
 645 650 655  
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala  
 660 665 670  
 Met Thr Gly Ala Leu Asn Ala Xaa Gly Glu Ile Glu Xaa Val Ser Phe  
 675 680 685  
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala  
 690 695 700  
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Xaa Asn Trp Ala Thr Phe  
 705 710 715 720  
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr  
 725 730 735  
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu  
 740 745 750

Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala  
 755 760 765  
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser  
 770 775 780  
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp  
 785 790 795 800  
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn  
 805 810 815  
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys  
 820 825 830  
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu  
 835 840 845  
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr  
 850 855 860  
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His  
 865 870 875 880  
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu  
 885 890 895  
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys  
 900 905 910  
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile  
 915 920 925  
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu  
 930 935 940  
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu  
 945 950 955 960  
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn  
 965 970 975  
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr  
 980 985 990  
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp  
 995 1000 1005  
 Glu Asp Leu Glu  
 1010

<210> 78  
 <211> 1012  
 <212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(1012)

<223> Sequence of IBDV polyprotein CEF94-PP

<400> 78

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Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
20 25 30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
35 40 45

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
50 55 60

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr  
65 70 75 80

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
85 90 95

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
100 105 110

Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
115 120 125

Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
130 135 140

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
145 150 155 160

Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly  
165 170 175

Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys  
180 185 190

Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile  
195 200 205

Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly  
210 215 220

Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu  
225 230 235 240

Ser Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val His Gly Leu Val  
245 250 255

Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile  
 260 265 270  
 Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn  
 275 280 285  
 Leu Leu Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro  
 290 295 300  
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln  
 305 310 315 320  
 Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr  
 325 330 335  
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val  
 340 345 350  
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val  
 355 360 365  
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val  
 370 375 380  
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu  
 385 390 395 400  
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr  
 405 410 415  
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu  
 420 425 430  
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile  
 435 440 445  
 Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro  
 450 455 460  
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
 465 470 475 480  
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
 485 490 495  
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
 500 505 510  
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln  
 515 520 525  
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly  
 530 535 540

Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro  
 545 550 555 560  
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn  
 565 570 575  
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro  
 580 585 590  
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val  
 595 600 605  
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp  
 610 615 620  
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu  
 625 630 635 640  
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala  
 645 650 655  
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala  
 660 665 670  
 Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe  
 675 680 685  
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala  
 690 695 700  
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe  
 705 710 715 720  
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr  
 725 730 735  
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu  
 740 745 750  
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala  
 755 760 765  
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser  
 770 775 780  
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp  
 785 790 795 800  
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn  
 805 810 815  
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys  
 820 825 830  
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu

835		840		845
Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr				
850		855		860
Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His				
865		870		875
Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu				
	885		890	895
Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys				
	900		905	910
Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile				
	915		920	925
Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu				
	930		935	940
Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu				
945		950		955
Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn				
	965		970	975
Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr				
	980		985	990
Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp				
	995		1000	1005
Glu Asp Leu Glu				
1010				

<210> 79

<211> 1012

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(1012)

<223> Sequence of IBDV polyprotein D6948-PP

<400> 79

Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
1 5 10 15

Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
20 25 30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
35 40 45

Val	Gly	Asp	Thr	Gly	Ser	Gly	Leu	Ile	Val	Phe	Phe	Pro	Gly	Phe	Pro		
	50					55					60						
Gly	Ser	Ile	Val	Gly	Ala	His	Tyr	Thr	Leu	Gln	Ser	Asn	Gly	Asn	Tyr		
	65				70					75					80		
Lys	Phe	Asp	Gln	Met	Leu	Leu	Thr	Ala	Gln	Asn	Leu	Pro	Ala	Ser	Tyr		
				85					90					95			
Asn	Tyr	Cys	Arg	Leu	Val	Ser	Arg	Ser	Leu	Thr	Val	Arg	Ser	Ser	Thr		
			100					105					110				
Leu	Pro	Gly	Gly	Val	Tyr	Ala	Leu	Asn	Gly	Thr	Ile	Asn	Ala	Val	Thr		
		115					120					125					
Phe	Gln	Gly	Ser	Leu	Ser	Glu	Leu	Thr	Asp	Val	Ser	Tyr	Asn	Gly	Leu		
	130					135					140						
Met	Ser	Ala	Thr	Ala	Asn	Ile	Asn	Asp	Lys	Ile	Gly	Asn	Val	Leu	Val		
	145				150				155					160			
Gly	Glu	Gly	Val	Thr	Val	Leu	Ser	Leu	Pro	Thr	Ser	Tyr	Asp	Leu	Gly		
			165						170					175			
Tyr	Val	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala	Ile	Gly	Leu	Asp	Pro	Lys		
			180					185					190				
Met	Val	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg	Pro	Arg	Val	Tyr	Thr	Ile		
		195					200					205					
Thr	Ala	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser	Gln	Tyr	Gln	Ala	Gly	Gly		
	210					215					220						
Val	Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	Thr	Ser	Leu		
	225				230					235					240		
Ser	Ile	Gly	Gly	Glu	Leu	Val	Phe	Gln	Thr	Ser	Val	Gln	Gly	Leu	Ile		
			245					250						255			
Leu	Gly	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	Ala	Val	Ile		
		260						265					270				
Thr	Arg	Ala	Val	Ala	Ala	Asp	Asn	Gly	Leu	Thr	Ala	Gly	Thr	Asp	Asn		
		275					280					285					
Leu	Met	Pro	Phe	Asn	Ile	Val	Ile	Pro	Thr	Ser	Glu	Ile	Thr	Gln	Pro		
	290				295						300						
Ile	Thr	Ser	Ile	Lys	Leu	Glu	Ile	Val	Thr	Ser	Lys	Ser	Gly	Gly	Gln		
	305				310					315					320		
Ala	Gly	Asp	Gln	Met	Ser	Trp	Ser	Ala	Ser	Gly	Ser	Leu	Ala	Val	Thr		
			325					330						335			



Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val  
 340 345 350  
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val  
 355 360 365  
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val  
 370 375 380  
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu  
 385 390 395 400  
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr  
 405 410 415  
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu  
 420 425 430  
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile  
 435 440 445  
 Arg Ala Leu Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro  
 450 455 460  
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
 465 470 475 480  
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
 485 490 495  
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
 500 505 510  
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln  
 515 520 525  
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Ile Leu Arg Gly  
 530 535 540  
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro  
 545 550 555 560  
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn  
 565 570 575  
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro  
 580 585 590  
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val  
 595 600 605  
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp  
 610 615 620  
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu

625		630		635		640
Ser Lys Asp Pro	Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala					
	645		650		655	
Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala						
	660		665		670	
Met Thr Gly Ala Leu Asn Ala Tyr Gly Glu Ile Glu Asn Val Ser Phe						
	675		680		685	
Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala						
	690		695		700	
Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Ser Asn Trp Ala Thr Phe						
	705		710		715	720
Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr						
		725		730		735
Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr Asp Leu						
		740		745		750
Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala						
		755		760		765
Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser						
		770		775		780
Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp						
		785		790		795
Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn						
		805		810		815
Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys						
		820		825		830
Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu						
		835		840		845
Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr						
		850		855		860
Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His						
		865		870		875
Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu						
		885		890		895
Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys						
		900		905		910
Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile						
		915		920		925

Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu  
 930 935 940

Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu  
 945 950 955 960

Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn  
 965 970 975

Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr  
 980 985 990

Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Ala Val Ser Asp  
 995 1000 1005

Glu Asp Leu Glu  
 1010

<210> 80

<211> 290

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(290)

<223> Sequence of IBDV polyprotein TY89-PP

<400> 80

Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr Leu Asn  
 1 5 10 15

Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His Leu Ala Leu  
 20 25 30

Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp Ala Val Arg  
 35 40 45

Ala Met Asp Ala Ala Ala Asn Val Asp Pro Leu Phe Arg Ser Ala Leu  
 50 55 60

Gln Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala  
 65 70 75 80

Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys Asn Phe Leu  
 85 90 95

Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly  
 100 105 110

Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala  
 115 120 125

Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly  
 130 135 140  
 Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly  
 145 150 155 160  
 Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu Ile Pro  
 165 170 175  
 Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu Lys Ser Arg  
 180 185 190  
 Leu Ala Ser Glu Glu Gln Val Leu Arg Ala Ala Thr Ser Ile Tyr Gly  
 195 200 205  
 Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala  
 210 215 220  
 Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met  
 225 230 235 240  
 Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg  
 245 250 255  
 Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Ser Gln Arg  
 260 265 270  
 Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp  
 275 280 285  
 Leu Glu  
 290

<210> 81  
 <211> 881  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(881)  
 <223> Consensus sequence of IBDV VP1, whereby the Xaa  
 indicator may be any amino acid

<400> 81  
 Met Ser Asp Xaa Phe Asn Ser Pro Gln Ala Arg Ser Xaa Ile Ser Ala  
 1 5 10 15  
 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu  
 20 25 30  
 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser  
 35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Xaa Leu Gln Pro  
 50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro  
 65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr  
 85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro  
 100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile  
 115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala  
 130 135 140

Xaa Xaa Xaa Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg  
 145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu  
 165 170 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro  
 180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile  
 195 200 205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro  
 210 215 220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp  
 225 230 235 240

Gly Xaa Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser  
 245 250 255

Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly  
 260 265 270

Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Xaa Leu  
 275 280 285

Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu  
 290 295 300

Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro  
 305 310 315 320

Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn  
 325 330 335

Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr

340										345										350										
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly															
			355					360						365																
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg															
	370					375					380																			
Ile	Val	Glu	Trp	Ile	Xaa	Ala	Pro	Xaa	Glu	Pro	Lys	Ala	Leu	Val	Tyr															
385					390				395						400															
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp															
			405						410					415																
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala															
			420					425					430																	
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met															
	435						440					445																		
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu															
	450					455					460																			
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr															
465					470				475					480																
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu															
				485					490					495																
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Xaa	Gln	Pro	Xaa	Pro															
			500					505					510																	
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe															
		515					520					525																		
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu															
	530					535					540																			
Val	Xaa	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu															
545					550					555				560																
Gln	Xaa	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr															
				565					570					575																
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg															
			580					585					590																	
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu															
		595					600					605																		
Lys	Ser	Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu															
	610					615					620																			
Ala	Leu	Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala															
625					630					635					640															

Cys Lys Asn Asn Ala Xaa Ala Ala Arg Arg His Leu Glu Ala Lys Gly  
 645 650 655  
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe  
 660 665 670  
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Xaa Glu  
 675 680 685  
 Ser Leu Ala Glu Leu Asn Xaa Pro Val Pro Pro Lys Pro Pro Asn Val  
 690 695 700  
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu  
 705 710 715 720  
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu  
 725 730 735  
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala  
 740 745 750  
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp  
 755 760 765  
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp  
 770 775 780  
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala  
 785 790 795 800  
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu  
 805 810 815  
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu  
 820 825 830  
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly  
 835 840 845  
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala  
 850 855 860  
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Xaa  
 865 870 875 880

Xaa

<210> 82  
 <211> 881  
 <212> PRT  
 <213> Infectious bursal disease virus  
 <220>

<221> DOMAIN

<222> (1)..(881)

<223> Sequence of IBDV CEF94-VP1

<400> 82

Met	Ser	Asp	Ile	Phe	Asn	Ser	Pro	Gln	Ala	Arg	Ser	Thr	Ile	Ser	Ala
1				5					10					15	

Ala	Phe	Gly	Ile	Lys	Pro	Thr	Ala	Gly	Gln	Asp	Val	Glu	Glu	Leu	Leu
			20					25					30		

Ile	Pro	Lys	Val	Trp	Val	Pro	Pro	Glu	Asp	Pro	Leu	Ala	Ser	Pro	Ser
		35					40					45			

Arg	Leu	Ala	Lys	Phe	Leu	Arg	Glu	Asn	Gly	Tyr	Lys	Val	Leu	Gln	Pro
	50					55					60				

Arg	Ser	Leu	Pro	Glu	Asn	Glu	Glu	Tyr	Glu	Thr	Asp	Gln	Ile	Leu	Pro
65					70					75					80

Asp	Leu	Ala	Trp	Met	Arg	Gln	Ile	Glu	Gly	Ala	Val	Leu	Lys	Pro	Thr
				85					90					95	

Leu	Ser	Leu	Pro	Ile	Gly	Asp	Gln	Glu	Tyr	Phe	Pro	Lys	Tyr	Tyr	Pro
			100					105					110		

Thr	His	Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile
		115					120						125		

Ala	Leu	Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala
	130					135						140			

Asn	Glu	Gly	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg
145					150						155				160

Asp	Lys	Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Thr	Arg	Leu
				165					170					175	

Val	Ala	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro
			180					185					190		

Leu	Lys	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile
		195					200						205		

Thr	Leu	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro
	210						215					220			

Leu	Thr	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp
225					230						235				240

Gly	Asp	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser
				245					250					255	

Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly
			260					265						270	



Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu		
		275					280					285					
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu		
	290					295					300						
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro		
305					310					315					320		
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn		
				325					330					335			
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr		
			340					345					350				
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly		
		355					360					365					
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg		
	370					375					380						
Ile	Val	Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr		
385					390					395					400		
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp		
			405						410					415			
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala		
			420					425					430				
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met		
		435					440					445					
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu		
	450					455					460						
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr		
465					470					475					480		
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu		
				485					490					495			
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro		
			500					505					510				
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe		
		515					520					525					
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu		
	530					535					540						
Val	Leu	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu		
545					550					555					560		

Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr  
 565 570 575  
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg  
 580 585 590  
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu  
 595 600 605  
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu  
 610 615 620  
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala  
 625 630 635 640  
 Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly  
 645 650 655  
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe  
 660 665 670  
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu  
 675 680 685  
 Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val  
 690 695 700  
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu  
 705 710 715 720  
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu  
 725 730 735  
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala  
 740 745 750  
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp  
 755 760 765  
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp  
 770 775 780  
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala  
 785 790 795 800  
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu  
 805 810 815  
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu  
 820 825 830  
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly  
 835 840 845  
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala

850                      855                      860  
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Gln  
 865                      870                      875                      880  
 Pro  
  
 <210> 83  
 <211> 879  
 <212> PRT  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> DOMAIN  
 <222> (1)..(879)  
 <223> Sequence of IBDV D6948-VP1  
  
 <400> 83  
 Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Lys Ile Ser Ala  
 1                      5                      10                      15  
 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu  
 20                      25                      30  
 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser  
 35                      40                      45  
 Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Ile Leu Gln Pro  
 50                      55                      60  
 Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro  
 65                      70                      75                      80  
 Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr  
 85                      90                      95  
 Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro  
 100                      105                      110  
 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile  
 115                      120                      125  
 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala  
 130                      135                      140  
 Thr Asp Asn Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg  
 145                      150                      155                      160  
 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu  
 165                      170                      175  
 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro  
 180                      185                      190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile  
 195 200 205  
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro  
 210 215 220  
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp  
 225 230 235 240  
 Gly Glu Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser  
 245 250 255  
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly  
 260 265 270  
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Ala Leu  
 275 280 285  
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu  
 290 295 300  
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro  
 305 310 315 320  
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn  
 325 330 335  
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr  
 340 345 350  
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly  
 355 360 365  
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg  
 370 375 380  
 Ile Val Glu Trp Ile Met Ala Pro Asp Glu Pro Lys Ala Leu Val Tyr  
 385 390 395 400  
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp  
 405 410 415  
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala  
 420 425 430  
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met  
 435 440 445  
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu  
 450 455 460  
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr  
 465 470 475 480  
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu



Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala  
 785 790 795 800  
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu  
 805 810 815  
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu  
 820 825 830  
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly  
 835 840 845  
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala  
 850 855 860  
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln  
 865 870 875

<210> 84  
 <211> 145  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(145)  
 <223> Consensus sequence of IBDV VP5, whereby the Xaa  
 indicator may be any amino acid

<400> 84  
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Xaa Pro Ala  
 1 5 10 15  
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
 20 25 30  
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Xaa Glu Ala His  
 35 40 45  
 Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
 50 55 60  
 Val Arg Ala Asn Cys Leu Phe Pro Trp Xaa Pro Trp Leu Asn Cys Gly  
 65 70 75 80  
 Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp  
 85 90 95  
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala  
 100 105 110  
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Xaa Trp Trp Arg

115 120 125  
 Leu Cys Thr Lys Xaa His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
 130 135 140

Glu  
 145

<210> 85  
 <211> 145  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(145)  
 <223> Sequence of IBDV D6948-VP5

<400> 85  
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Glu Pro Ala  
 1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
 20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Arg Glu Ala His  
 35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
 50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp Leu Asn Cys Gly  
 65 70 75 80

Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp  
 85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala  
 100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Pro Trp Trp Arg  
 115 120 125

Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
 130 135 140

Glu  
 145

<210> 86  
 <211> 145  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(145)

<223> Sequence of IBDV CEF94-VP5

<400> 86

Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala  
1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His  
35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly  
65 70 75 80

Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp  
85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala  
100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg  
115 120 125

Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
130 135 140

Glu

145

<210> 87

<211> 149

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(149)

<223> Sequence of IBDV D6948-VP5

<400> 87

Met Leu Ser Leu Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp  
1 5 10 15

Asp Glu Pro Ala Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu  
20 25 30



Pro	Ser	Asp	Ala	Asn	Asn	Arg	Thr	Gly	Val	His	Ser	Gly	Arg	His	Pro
		35					40					45			
Arg	Glu	Ala	His	Ser	Gln	Val	Arg	Asp	Leu	Asp	Leu	Gln	Phe	Asp	Cys
	50					55					60				
Gly	Gly	His	Arg	Val	Arg	Ala	Asn	Cys	Leu	Phe	Pro	Trp	Phe	Pro	Trp
65					70					75					80
Leu	Asn	Cys	Gly	Cys	Ser	Leu	His	Thr	Ala	Glu	Gln	Trp	Glu	Leu	Gln
			85					90						95	
Val	Arg	Ser	Asp	Ala	Pro	Asp	Cys	Pro	Glu	Pro	Thr	Gly	Gln	Leu	Gln
			100					105					110		
Leu	Leu	Gln	Ala	Ser	Glu	Ser	Glu	Ser	His	Ser	Glu	Val	Lys	His	Thr
		115					120					125			
Pro	Trp	Trp	Arg	Leu	Cys	Thr	Lys	Trp	His	His	Lys	Arg	Arg	Asp	Leu
	130					135					140				
Pro	Arg	Lys	Pro	Glu											
145															